

-1- TISSUE SPECIFICITY: Expression levels are very low or not detectable on monocytes, T-cells, B-cells, dendritic cells and natural killer (NK) cells.

-1- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.

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CC	EMBL; AP025531; AAB87665; 1;	Db	197 AYDNSPPVWSLPSDLLBLVPGVSKKPSLSSVQPPMVAEGESLTLCQCVSDVGTDRLVLY 256
CC	DR EMBL; BC017412; AAH17412; 1; -;	Qy	241 KEGERDFLQRGWPQOAGLSQANFTLGPGVSPSPSGQYRCYS SAHNLSSEN SAP SDPLDIL 300
CC	DR HSSP; P43626; 1NKR.	Db	257 KEGERDFLQRGWPQOAGLSQANFTLGPGVSPSPSGQYRCYS SAHNLSSEN SAP SDPLDIL 316
CC	Genev; HGNC:6613; LLRA2.	Qy	301 TGQYDPRPSLSVQPVPTVAPGKNTLLCOSRGQTFLTLKEG 343
CC	MIM; 604812; -;	Db	317 TGQYDPRPSLSVQPVPTVAPGKNTLLCOSRGQTFLTLKEG 359
CC	DR InterPro; IPR07110; Ig-like.		
CC	DR InterPro; IPR03598; Ig_ Ig-like.		
CC	DR Pfam; PF00047; ig; 3.		
CC	DR PROSITE; PS50835; Ig_LIKE; 2.		
CC	KW Immune response; Receptor; Repeat; Signal; Transmembrane;		
CC	KW Immunoglobulin domain; Glycoprotein; Antigen; Alternative splicing;		
CC	KW Polymorphism; Multigene family.		
FT	FT SIGNAL; 1	POTENTIAL.	
FT	FT CHAIN	23	
FT	FT DOMAIN	24	449
FT	FT TRANSMEM	24	483
FT	FT DOMAIN	450	470
FT	FT DOMAIN	471	483
FT	FT DOMAIN	27	113
FT	FT DOMAIN	117	222
FT	FT DOMAIN	224	313
FT	FT DOMAIN	324	413
FT	FT DISUFDID	49	97
FT	FT DISUFDID	143	195
FT	FT DISUFDID	244	295
FT	FT DISUFDID	344	395
FT	PT CARBOHYD	64	64
FT	PT CARBOHYD	103	103
FT	PT CARBOHYD	138	138
FT	PT CARBOHYD	279	279
FT	PT CARBOHYD	300	300
FT	PT CARBOHYD	339	339
FT	PT CARBOHYD	429	429
FT	PT VARSPLIC	419	436
FT	VARIANT	25	25
FT	VARIANT	25	25
FT	SEQUENCE	483	AA;
SQ	SEQUENCE	529911	MW;
Query Match	Best Local Similarity	100.0%	; score 1868; DB 1; Length 483;
Matches 343; Conservative 0; Mismatches 0; Gaps 0;			
Qy	1 PRTHVDAGLHAKPTWAEPGSVTIQGSPVTLRCQGSLQAEYHLYRENKSASWYRIQEP 60	61 GKNGQPIPSPITWEHAGRHCQQYSHHSSEYSDPELVTVTGSKPTLALSPTVTLG 120	
Db	17 PRTHVDAGLHAKPTWAEPGSVTIQGSPVTLRCQGSLQAEYHLYRENKSASWYRIQEP 76	77 GKNGQPIPSPITWEHAGRHCQQYSHHSSEYSDPELVTVTGSKPTLALSPTVTLG 136	
Qy	21 GNVTLQCVSQVAFGFLCKEGEDDEFQRQLNSHSHRGWSWAFSFGPVSPSRMSYRCY 180	137 GNVTLQCVSQVAFGFLCKEGEDDEFQRQLNSHSHRGWSWAFSFGPVSPSRMSYRCY 196	
Db			
Qy	181 AYDNSPPVWSLPSDDLLBLVPGVSKKPSLSSVQPGPMVAEGESLTLCQCVSDVGTDRLVLY 240		

Result No.	Score	Query	Match	Length	DB ID	Description
1	1868	100.0	483	1	LIA2_HUMAN	Q8n149 homolog (ortholog), human
2	1475	79.0	439	1	LIA3_HUMAN	Q8ng68 homolog (ortholog), human
3	1458	78.1	489	1	LIA1_HUMAN	Q8n019 homolog (ortholog), human
4	1457	78.0	598	1	LIB2_HUMAN	Q8nh16 homolog (ortholog), human
5	1455	77.7	650	1	LIB1_HUMAN	Q8n022 homolog (ortholog), human
6	1192	63.8	631	1	LIB3_HUMAN	Q8n023 homolog (ortholog), human
7	1073	57.7	499	1	LIA4_HUMAN	Q8mjt7 pan-trogloboid
8	1073	57.4	590	1	LIB5_PANTR	Q8mjt7 pan-trogloboid
9	1071	57.3	643	1	LIB6_PANTR	Q8mjt7 pan-trogloboid
10	521	27.9	444	1	K3L1_HUMAN	Q14943 homolog (ortholog), killer cell
11	512	27.4	387	1	K3L1_HUMAN	Q8nb16 homolog (ortholog), killer cell
12	499	26.7	448	1	LIB4_HUMAN	Q8n024 homolog (ortholog), killer cell
13	492	26.3	455	1	K3L2_HUMAN	Q8n025 homolog (ortholog), killer cell
14	461	24.7	432	1	K3L1_MOUSE	Q83556 rat
15	454	24.3	335	1	G49B_MOUSE	Q83556 rat
16	445	23.8	422	1	K3L1_RAT	Q83556 rat
17	403	21.6	303	1	G49A_MOUSE	Q61450 mouse
18	387	20.7	304	1	K2S4_HUMAN	Q83532 homolog (ortholog), mouse
19	385	20.6	304	1	K2S2_HUMAN	Q83621 homolog (ortholog), mouse
20	383	20.5	348	1	K2L1_HUMAN	Q83226 homolog (ortholog), mouse
21	382	20.5	341	1	K2L3_HUMAN	Q84281 homolog (ortholog), mouse
22	370	19.8	304	1	K2S1_HUMAN	Q14554 homolog (ortholog), mouse
23	370	19.8	348	1	K2L2_HUMAN	Q83227 homolog (ortholog), mouse
24	365	19.5	377	1	K2L4_HUMAN	Q99706 homolog (ortholog), mouse
25	359	19.2	304	1	K2S3_HUMAN	Q83522 homolog (ortholog), mouse
26	358	19.2	304	1	K2S5_HUMAN	Q14553 homolog (ortholog), mouse
27	307	16.5	287	1	FCAR_HUMAN	P24071 homolog (ortholog), mouse
28	243	13.0	495	1	AIBG_HUMAN	P82427 homolog (ortholog), mouse
29	216	11.6	291	1	DMD3_DIDMR	P82457 homolog (ortholog), mouse
30	178	9.5	3707	1	PGBM_MOUSE	Q05793 homolog (ortholog), mouse
31	155	8.3	4391	1	PGBM_HUMAN	P20733 homolog (ortholog), mouse
32	154	8.3	847	1	CD22_HUMAN	P14781 homolog (ortholog), mouse
33	149	8.0	526	1	CEA1_HUMAN	

ALIGNMENTS						
RESULT 1						
LIA2_HUMAN						
ID	LIA2_HUMAN	STANDARD;	PRT;	483	AA.	
AC	Q8N149; O75020;					
DT	10-OCT-2003 (Rel. 42, Created)					
DT	10-OCT-2003 (Rel. 42, Last sequence update)					
DT	10-OCT-2003 (Rel. 42, Last annotation update)					
DE	Leukocyte immunoglobulin-like receptor subfamily A member 2 precursor (Leucocyte immunoglobulin-like receptor 7) (LIR-7) (Immunoglobulin-like transcript 1) (ILR-1) (CD85 antigen).					
DB	LIRR2 OR LIR7 OR ILR1.					
GN	"A family of human lymphoid and myeloid Ig-like receptors, some of which bind to MHC class I molecules."					
RN	J. Immunol. 159:5192-5196 (1997).					
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIALITY.					
RC	TISSUE=Peripheral blood leukocytes;					
RX	MEDLINE=8820834; PubMed=1548455;					
RA	Borges L., Hsu M.-L., Fanger N., Kubin M., Cosman D. <i>In vitro</i> characterization of human lymphoid and myeloid Ig-like receptors, some of which bind to MHC class I molecules.					
RT	"A family of human lymphoid and myeloid Ig-like receptors, some of which bind to MHC class I molecules."					
RL	[1]					
RN	[2]					
RP	SEQUENCE FROM N.A. (ISOFORM 2).					
RC	TISSUE=lung, and Pancreas;					
RX	MEDLINE=22388257; PubMed=12477932;					
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Shamma C.M., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Aleschul S.P., Zeeberg B., Buetow K.H., Bhattacharyya P.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Rubin G.M., Brownstein M.J., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E., Blakesley R.W., Loquellano N.A., Peters G.J., Abramson R.D., Mullayah S.J., Bosak S.A., McEwan P.J., McLaren K.J., Malek J.A., Richards S., Worley K.C., Sodergren E.J., Hale S., Garcia A.M., Gay L.J., Hale S., Villalon D.K., Muñiz D.M., Gibbs R.A., Fahey J., Hallon B., Kettenbach M., Madan A., Madan K., Shevchenko A., Whiting M., Madan A., Young A.C., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Kozlowski M.I., Skalska U., Schnarch A., Schein J.B., Jones S.J.M., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";					
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).					
CC	-/- FUNCTION: May act as receptor for class I MHC antigens.					
CC	-/- SUBCELLULAR LOCATION: Type I membrane protein.					
CC	-/- ALTERNATIVE PRODUCTS:					
CC	Event=Alternative splicing; Named isoforms=2; Name=1; IsoID=Q8N149-1; Sequence=Displayed;					
CC	IsoID=Q8N149-2; Sequence=YSP 008455;					
CC	Note=No experimental confirmation available;					